Letter

Combat with emerging infectious diseases: Clinicians should do better

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Summary: In the spring of 2013, an emerging infectious disease emerged in China, 132 cases of human were infected with the H7N9 avian influenza virus, 39 cases were resulted in death within 3 month, which sparked a global concern about public health. Many reports have been published about this disease, including clinical characteristics and genomic information. However, more emerging infectious disease may infect human in the future. Confronted with the escalating scale of compounding probabilities, physicians or clinicians as the first line that meet patients who suffering from emerging infectious disease, we should do better by using our intellect and strong will to carry out public health measures, biomedical research, and technological advances.

Globally, infectious diseases are the second leading cause of death (following cardiovascular disease), but the leading cause of mortality among young people (under the age of 50) overwhelmingly (1). According to the World Health Organization, infectious diseases accounted for about 26% of the 57 million deaths worldwide (2).

Emerging infectious diseases (EIDs) are infectious disease whose incidence has increased in the past 35 years and may increase in the near future which account for about 12% of all human pathogens (3). EIDs are caused by newly identified species or strains that may have evolved from a known infection (*e.g.* influenza) or spread to a new population or areas undergoing ecologic transformation, or reemerging. Of growing concern are adverse synergistic interactions between

emerging diseases and other communicable and noncommunicable conditions leading to the development of novel epidemics. A criterion was given by the U.S. Centers for Disease Control and Prevention (CDC) that identifies the following factors contributing to disease emergence: microbial adaption, changes in human susceptibility, *etc*.

From March 31 to May 31, 2013, 132 cases of human were infected with the H7N9 avian influenza virus in China, 39 cases were resulted in death, which sparked global concerns about public health (4,5), and many reports have been published. As a clinician in front line to combat with H7N9 infection in Shanghai, our research group has also published some papers about this emerging infectious disease, especially about its clinical characteristic (6). Now I would like to illustrate some of the lessons we have learned as we combat the emerging infectious disease – the avian influenza H7N9 – with the purpose of providing references for other clinicians and researchers to face crisis that will continue to haunt mankind in the future.

On February 26, 2013, I was invited to go to the Fifth People's Hospital, Min-hang District, Shanghai, affiliated to Fudan University and took part in a clinical consultation. Three members of a family, the father and his two sons were suffering from severe pneumonia and had been hospitalized, one of which was on the verge of death. The onset of unknown disease in this family was located between February 11 and February 20, 2013. High fever and severe pneumonia developed 1 week after the onset of illness, of which interstitial lung disease was considered initially. Multiple organ failure appeared 7-9 days later, with low white blood cells and dramatically decreased in platelets. He had no known history of exposure to live birds during the 2 weeks before the onset of symptoms. Sputum and sera from patients were sent to district CDC, Shanghai for identification of common subtypes of influenza virus,

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chlamydia, mycoplasma and bacteria which had been confirmed negative later on. Based upon these typical manifestations, infectious viral pneumonia was taken into my consideration. So I decided to use anti-viral drug, Oseltamivir, immediately, the dosage would be as twice as normal. Meanwhile, as I asked, all specimens had been sent to our lab, Shanghai Public Health Clinical Center affiliated to Fudan University in which P3 laboratory was available. After real-time RT-PCR test, viral isolation, and full genome sequencing, two of the three patients were infected with a novel avianorigin influenza A (H7N9) virus (7), and the results have been confirmed by China CDC.

As we all know, multiple factors, including economic development, climate changes and land use, human demographics and behavior, and international travel and commercial activities, contribute to the emergence and reemergence of infectious diseases (8,9). As basic or laboratory scientists know, genomics has played a critical role in basic research in infectious diseases. Nowadays, an unknown pathogen can often be identified and sequenced within days. The ability to sequence microbes has taken its place at the forefront of how we handle with emerging infections. Fundamental research underlies almost everything we do in studying and responding to infectious diseases. From understanding pathogenesis, virulence factors, patterns of transmission, and host susceptibility, to developing new technologies and countermeasures such as vaccines, therapeutic measures, and diagnostics.

However, physicians or clinicians are the first line that can meet patients who suffering from unidentified disease. We will never forget the epidemic of severe acute respiratory syndrome (SARS), for which it costed a very heavy and painful price 10 years ago (10), including reported clinician's victims (11,12). Over the past few years, more influenza strains have emerged with the capability of infecting humans (13, 14)and more emerging infectious disease will infected in the future. The H5N1 strain likely evolved from a few flocks of chickens in Hong Kong to the situation today where it has infected numerous flocks, as well as wild birds throughout Southeast Asia (15). Now we are confronted with what I call an escalating scale of compounding probabilities. If a few birds are infected, there is a problem, but not a big one. When more birds get infected, the problem will get bigger. When the virus is transmitted to humans, the problem is getting even worse. If it jumps to significant numbers of humans, the threat becomes a lethal one.

In our battle with emerging infectious diseases, we have a number of weapons in our armamentarium. Most important, we have an intellect and a strong will. We use these to carry out public health measures, biomedical research, and technological advances. I was proud to do it instead of being asked to do this, because a clinician can do better.

References

- Fauci AS. Emerging and reemerging infectious diseases: The perpetual challenge. Acad Med. 2005; 80:1079-1085.
- Many countries hit by health threats from both infectious and chronic diseases new data site makes WHO data and analyses widely available. Cent Eur J Public Health. 2011; 19:72.
- Del Rey Calero J. Emerging and reemerging infectious diseases. An Med Interna. 2002; 19:443-445.
- Song PP, Xia JF, Gao JJ, Xu LZ, Huang Y, Yao LN, Tang W. Measures to combat H7N9 virus infection in China: Live poultry purchasing habits, poultry handling, and living conditions increase the risk of exposure to contaminated environments. Biosci Trends. 2013; 7:168-171.
- Mei L, Song P, Tang Q, Shan K, Tobe RG, Selotlegeng L, Ali AH, Cheng Y, Xu L. Changes in and shortcomings of control strategies, drug stockpiles, and vaccine development during outbreaks of avian influenza A H5N1, H1N1, and H7N9 among humans. Biosci Trends. 2013; 7:64-76.
- Lu S, Xi X, Zheng Y, Cao Y, Liu X, Lu H. Analysis of the clinicalcharacteristics and treatment of twopatients with avian influenza virus (H7N9). Biosci Trends. 2013; 7:109-112.
- Gao R, Cao B, Hu Y, *et al.* Human infection with a novel avian-origin influenza A (H7N9) virus. N Engl J Med. 2013; 368:1888-1897.
- Weiss RA, McMichael AJ. Social and environmental risk factors in the emergence of infectious diseases. Nat Med. 2004; 10:S70-S76.
- Church DL. Major factors affecting the emergence and re-emergence of infectious diseases. Clin Lab Med. 2004; 24:559-586, v.
- From SARS to H7N9: Will history repeat itself? Lancet. 2013; 381:1333.
- 11. Penciner R. I am a SARS physician. CJEM. 2003; 5:281-282.
- Wu EB, Sung JJ. Haemorrhagic-fever-like changes and normal chest radiograph in a doctor with SARS. Lancet. 2003; 361:1520-1521.
- Lu S, Zheng Y, Li T, Hu Y, Liu X, Xi X, Chen Q, Wang Q, Cao Y, Wang Y, Zhou L, Lowrie D, Bao J. Clinical findings for early human cases of influenza A(H7N9) virus infection, Shanghai, China. Emerg Infect Dis. 2013; 19:1142-1146.
- Gao HN, Lu HZ, Cao B, *et al.* Clinical findings in 111 cases of influenza A (H7N9) virus infection. N Engl J Med. 2013; 368:2277-2285.
- World Health Organization. Avian influenza in humans. http://www.who.int/influenza/human_animal_interface/ avian_influenza/en/ (accessed on September 9, 2013)

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